Diversity Journal
ISSN 2525-5215
Volume 9, Number 2 (apr./jun. 2024) p. 0649 – 0659
https://diversitasjournal.com.br/diversitas_journal

Caracterização morfológica, divergência genética e seleção de genitores de batata doce para cruzamentos

Morphological characterization, genetic divergence and selection of sweet potato parents for hybridization

DANTAS, Adrielly Cabral⁽¹⁾; CAVALCANTE, Marcelo⁽²⁾; SILVA, Matheus Victor dos Santos⁽³⁾; SANTOS, Jamerson de Melo Silva⁽⁴⁾

(1) 0000-0001-9542-8015; Instituto Federal de Alagoas – Campus Maragogi. Maragogi, Graduação Tecnológica em Horticultura. Alagoas (AL), Brasil. acd2@aluno.ifal.edu.br.

(2) 0000-0002-0722-0618; Instituto Federal de Alagoas – Campus Maragogi, Curso Técnico em Agroecologia. Maragogi, Alagoas (AL), Brasil. marcelo.cavalcante@ifal.edu.br.

(3) 0009-0008-8879-9430; Instituto Federal de Alagoas – Campus Maragogi, Curso Técnico em Agroecologia. Maragogi, Alagoas (AL), Brasil. mvss27@aluno.ifal.edu.br.

(4) 0009-0007-6469-1858; Instituto Federal de Alagoas – Campus Maragogi, Curso Técnico em Agroecologia. Maragogi, Alagoas (AL), Brasil. jmss26@aluno.ifal.edu.br.

ABSTRACT

Studies on the genetic divergence of the base population, as well as the characterization of the genotypes are essential in the selection of parents within a breeding programme. Therefore, this research aimed at the morphological characterization of 33 sweet potato genotypes, the estimation of genetic divergence and the indication of parents for biparental crossing. Fourteen characteristics of the shoot and 11 of the roots were evaluated using morphological descriptors. Genetic divergence was estimated by the Tocher clustering test, using the Gower algorithm to calculate dissimilarity measures. A wide morphological variability was observed between the genotypes, both in the shoot and in the roots (length, diameter, shape, pigmentation, coloration). Root epidermis color ranged from cream, pinkish to reddish purple; the pulp color ranged from cream to dark purple. The morphological descriptors of shoots and roots showed the existence of genetic divergence, with the formation of six groups of similarity between the evaluated genotypes, allowing the indication of biparental crosses ‘CL 28 x Beterraba 1’, ‘CL 28 x Pão’, ‘CL 15 x Beterraba 1’, ‘CL 15 x Pão’, ‘CL 28 x F-16’, ‘CL 15 x F-16’, ‘CL 28 x F-15’, ‘CL 15 x F-15’, ‘F-15 x Beterraba 1’, ‘F-16 x Beterraba 1’, ‘F-15 x Pão’, ‘F-16 x Pão’, allowing gains with greater heterosis and superior progenies.

RESUMO

Estudos sobre a divergência genética da população base, bem como a caracterização dos genótipos são essenciais na seleção de genitores dentro de um programa de melhoramento genético. Portanto, esta pesquisa objetivou a caracterização morfológica de 33 genótipos de batata doce, a estimativa da divergência genética e a indicação de genitores para cruzamento biparentais. Foram avaliadas 14 características da parte aérea e 11 das raízes por meio de descritores morfológicos. A divergência genética foi estimada pelo teste de agrupamento Tocher, utilizando-se o algoritmo de Gower para o cálculo das medidas de dissimilaridade. Observou-se ampla variabilidade morfológica entre os genótipos, tanto na parte aérea, quanto nas raízes (comprimento, diâmetro, formato, pigmentação, coloração). A cor da epiderme da raiz variou do creme, rosado ao roxo avermelhado; já a cor da polpa variou de creme ao roxo escuro. Os descritores morfológicos da parte aérea e das raízes evidenciaram a existência de divergência genética, com a formação de seis grupos de similaridade entre os genótipos avaliados, possibilitando a indicação dos cruzamentos biparentais ‘CL 28 x Beterraba 1’, ‘CL 28 x Pão’, ‘CL 15 x Beterraba 1’, ‘CL 15 x Pão’, ‘CL 28 x F-16’, ‘CL 15 x F-16’, ‘CL 28 x F-15’, ‘CL 15 x F-15’, ‘F-15 x Beterraba 1’, ‘F-16 x Beterraba 1’, ‘F-15 x Pão’, ‘F-16 x Pão’, possibilitando ganhos com maior heterose e progênies superiores.

ARTICLE INFORMATION

Article process:
Submitted:10/08/2023
Approved: 05/09/2024
Published: 05/11/2024

Keywords:
Ipomoea batatas, genetic variability, morphological descriptors, multivariate analysis

Palavras- chave:
Ipomoea batatas, variabilidade genética,descritores morfológicos, análise multivariada

Doi: 10.48017/dj.v9i2.2800

Introduction

Sweet potato (*Ipomoea batatas* L. Lam.), belonging to the Convolvulaceae family, originated in Central America (Srisuwan et al., 2006), is a species cultivated worldwide (Bovell-Benjamin, 2007), in which China is the largest producer, responsible for 54.9% of world production (49.2 Mt). Brazil ranks 15th, with 847.9 thousand tons produced in 59.5 thousand hectares (FAO, 2020). The first plants were introduced in Brazil in the sixteenth century (Austin, 1987), adapting to different biomes, being cultivated in all states, with São Paulo (32.8%), Rio Grande do Sul (13.6%) and Sergipe (9.2%) standing out as the largest producers (IBGE, 2020a).

Allogamy, present in the species, due to the mechanisms of self-incompatibility and sterility (Indriani et al., 2021), promotes a high degree of heterozygosity to the germplasm, reflecting in wide genetic variability for different phenotypic descriptors (Ritschel, 1998), both of the root (number, shape, weight, color of the epidermis and pulp) (Silva et al., 2012), and shoot (length of the stems, color, shape, and number of leaves) (Azevedo et al., 2019).

In genetic breeding programs, the development of new cultivars depends on the presence of divergent genotypes in the base population. Therefore, estimating genetic divergence, regardless of the method (morphological, molecular, or enzymatic markers), will allow the quantification of genotypic distances, enabling the indication of crosses, seeking to obtain maximum heterosis (Cruz et al., 2020). In sweet potato, being an allogamous species, the crosses can be biparental or multiple, generating full-sib and half-siblings progenies, respectively.

Family farming is responsible for 59% of the production of sweet potatoes in Brazil (IBGE, 2020a), and the low technological level used in plantations is not uncommon, considering the low level of education, the lack of technical assistance (91.8% are not assisted) and the deficient management (52.1% do not fertilize) (IBGE, 2020b). These factors limit productivity and increase the number of non-commercial roots (Silva et al., 2015), with losses in marketing, both on the part of wholesalers, who tend to reduce the price, and on the part of consumers, who reject part of the product exposed for sale (Fernandes et al., 2021). Therefore, it is necessary that breeding programs consider not only the agronomic characteristics, but also the technological level employed by the producers.

The objective of this research was to characterize 33 sweet potato genotypes, estimate genetic divergence and indicate parents for biparental crosses.

Material and Methods

The research was carried out at the Federal Institute of Alagoas - Maragogi Campus, in the 2022/2023 biennium, under the coordinates 8° 56' 42" E and 35° 10' 25" W. The climate of the region is of the 'As' type, tropical rainy, according to the Köppen classification, with annual averages of temperature, precipitation and relative humidity of 27°C, 1,144 mm and 80%, respectively (Climate-Date, 2023).

A total of 33 genotypes were evaluated, in which the clones (CL) were obtained from crosses conducted by the Genetic Improvement Program of the Federal University of Alagoas, described below: CL 26, CL 28, CL 39 and CL 40, from the Coquinho variety (♀); CL 10, CL 15, CL 17, CL 18 and CL 22, from the cross between '♀Coquinho x ♂CL 6'; CL 31, from clone CL 14 (♀); botanical families F-01, F-04, F-05, F-09, F-10, F-11, F-14, F-15 and F-18; Amendoin, Campina 1, Campina 2, Canela, Copinha Rosa, Bem Cuia, Beterraba, Gaita, Mãe de Família, Pão, Rainha da Praia, Rainha de Penedo, Roxinha and Tinguá landraces, from different regions of Alagoas and Pernambuco.

On October 17, 2022, the germplasm bank was formed by planting two 30 cm branches of each genotype, in 20-liter plastic buckets allocated under field conditions, containing soil and filter cake as substrate in a 3:1 ratio. Irrigation, when necessary, was carried out by means of a micro-sprinkler system, in the morning (10:00 am) and afternoon (3:00 pm).

At 90 days after planting (DAP), 14 morphological descriptors of the shoot (length of the main stem, diameter and length of the internode, color of the main stem, shape and length of the leaf, pigmentation of the vein, color of the mature and immature leaf, length and pigmentation of the petiole, type, number and shape of the lobe) were evaluated, obtained in the central region of the main stem, in fully expanded sheets. At 150 DAPs, 11 descriptors were evaluated, considering all roots (weight, number, diameter and length, cortex thickness, root shape, surface defect, epidermis and pulp color, presence of latex, and incidence of pest damage), following the recommendations of Huáman (1991). For the measurements, a tape measure, a digital caliper and a digital analytical scale were used. The color pattern of the epidermis and root pulp was performed according to the Munsell Color Chart (Munsell, 1975).

With the data, the genetic divergence was estimated using Tocher's multivariate clustering test, using Gower's algorithm to calculate the dissimilarity measures, based on quantitative and qualitative variables. The cophenetic correlation coefficient was applied to determine the robustness of the cluster, using the Mantel test ($p<0.05$). For all analyses, the Genes software was used, version 1990.2023.66 (Cruz et al., 2013).

Results and Discussion

Variability was observed in all quantitative descriptors of the shoot evaluated (Table 1), especially the internode length, which ranged from 1.3 (F-15 family) to 12.3 cm (Pão variety), with a coefficient of variation of 58.3%, considered of high magnitude (Ferreira, 2018). The high coefficient of variation may be the indicator of the existence of genetic variability in segregating genotypes, according to Cavalcante & Costa (2021). Among the qualitative descriptors, petiole pigmentation, with six categories, showed the greatest variation. The presence of a genotype (Pão variety) with purple coloration was also highlighted, especially in the leaves, due to the presence of anthocyanins, responsible for the antioxidant action that, when consumed, may be beneficial to human health (Nguyen et al., 2021), which is a characteristic of interest for the development of new cultivars.

Table 1.

Morphological characterization of the shoot of 33 sweet potato genotypes

Genotypes	LMS (cm)	ID (mm)	IL (cm)	CS	MLS	SL (cm)	VP	MLC	ILC	PL	PP	LT	LN	LS
Amendoim	89	6.9	7.0	1	6	9.1	2	2	2	3	1	5	3	4
Bem Cuia	71	5.4	1.7	1	6	9.9	2	2	2	3	1	5	5	4
Beterraba 1	69	6.6	1.8	1	3	8.5	2	2	3	3	1	1	0	2
Campinas 1	180	6.3	3.6	1	6	8.2	5	2	6	3	5	5	3	4
Campinas 2	125	5.6	9.8	1	6	7.7	7	2	2	3	1	5	3	4
Canela	83	6.4	2.7	1	6	10.3	7	2	3	3	4	5	3	2
CL 10	65	6.6	2.0	1	6	10.0	2	2	2	5	1	5	3	4
CL 15	121	5.5	5.1	1	6	20.1	2	2	3	5	1	5	3	4
CL 17	185	5.6	4.8	1	3	10.0	8	2	2	3	5	1	0	1
CL 18	125	4.4	2.6	1	7	7.4	2	2	2	3	1	7	5	5
CL 22	110	8.8	8.3	1	6	28.5	7	2	3	9	4	5	3	4
CL 26	200	5.5	6.4	1	6	12.1	8	2	3	3	2	5	3	4
CL 28	233	6.3	4.6	1	6	7.7	8	2	2	3	5	5	3	4
CL 31	136	7.1	3.0	1	3	8.8	4	2	6	3	5	1	0	1
CL 39	184	4.9	6.8	1	7	9.4	2	2	2	3	1	7	5	5
CL 40	68	7.4	4.2	1	3	26.3	2	2	2	1	1	1	0	1
Cop. Rosa	73	4.6	2.6	1	6	9.1	2	2	3	3	1	5	3	4
F-01	58	8.7	2.1	1	6	10.2	2	2	2	3	1	5	3	4
F-04	127	6.2	4.6	1	5	10.2	2	2	3	3	1	5	3	4
F-05	90	5.2	3.0	1	6	9.7	2	2	3	3	1	5	3	4
F-09	200	8.6	3.6	1	5	12.3	8	2	2	3	1	5	3	4
F-10	90	5.5	3.1	1	3	9.7	8	2	2	3	5	1	0	1
F-11	86	6.7	2.4	1	6	9.1	2	2	2	3	1	5	3	4
F-14	64	6.1	2.0	1	7	8.9	7	2	2	3	3	7	5	5
F-15	73	6.1	1.3	1	6	10.0	2	2	3	3	1	5	5	4
F-16	170	5.4	2.8	1	6	9.8	2	2	2	3	1	5	3	4
Gaia	153	10.4	5.8	1	3	24.5	2	2	3	5	1	1	0	1
M. Família	228	6.2	9.3	1	7	23.6	5	2	3	5	5	7	5	5
Pão	65	5.9	12.3	7	6	22.8	8	9	3	7	9	5	3	4
R. Praia	64	7.2	5.3	1	6	29.4	2	2	2	5	1	5	3	4
R. Penedo	180	7.0	3.2	1	6	10.6	8	2	2	3	9	7	5	4
Roxinha	91	6.1	4.0	1	3	9.1	8	2	2	3	5	1	0	1
Tinguá	223	8.4	5.5	1	3	9.6	5	2	3	3	3	1	0	1
CV (%)	45.5	20.4	58.3	--	--	52.1	--	--	--	--	--	--	--	--

Note: LMS: length of main stem; ID: internode diameter; IL: internode length; CS: color of the main stem; MLS: mature leaf shape; SL: sheet length; VP: vein pigmentation; MLC and ILC: mature and immature leaf color; PL and PP: petiole length and pigmentation; LT, LN and LS: lobe type, number and shape. CV (%): coefficient of variation.

Following the classification of Huamán (1991), 36.4 and 33.3% of the genotypes had semi-erect (75 – 150 cm) and spread (150 – 250 cm) stems, respectively (Table 1), which is a characteristic directly linked to plant spacing, causing smaller stands (plants/ha), which can reduce commercial root yield (Melo et al., 2019). On the other hand, the shoot may have high yield and can be used for animal feed.

The internode length was very short for 42.4% of the genotypes (score 1, <3.0 cm; Bem Cuia, Beterraba 1, Canela, CL 10, CL 18, CL 31, Copinha Rosa, F-01, F-05, F-11, F-14, F-15, F-16, Pão and F-05 genotypes), short for 39.4% (score 3, between 3.1 – 6.0 cm; Campinas 1, CL 15, CL 17, CL 28, CL 40, F-04, F-09, F-10, Gaia, Rainha de Penedo, Rainha da Praia, Roxinha and Tinguá genotypes) and intermediate for 18.2% (score 5, between 6.1 – 9.0 cm; Amendoim, CL 22, CL 26 and CL 39 genotypes), respectively (Table 1). This is an important characteristic that is directly linked to planting, considering that Perrud et al. (2021) observed that stems containing 8 to 10 buds, buried above and below ground, provided greater number and production of commercial roots.

The internode diameter ranged from 4.4 to 10.4 mm, for the clone CL 18 and Gaita variety, respectively, in which 72.7% of the genotypes had fine diameter (between 4 - 6 mm; Huamán, 1991). Considering that the main form of propagation of the crop occurs by means of stems, thin internodes may be more susceptible to breakage at the time of planting (Cavalcante et al., 2008). On the other hand, this characteristic may offer an advantage regarding the preference of the root borer (*Megastes pusialis* Snellen), since it cannot complete its cycle inside the stems, due to the insufficient diameter for cocoon formation (Cavalcante et al., 2009). The color of the main branch was predominantly green for 32 genotypes, especially the Pão variety, with a dark purple color (Table 1).

For leaf shape, the following types were cordiform (score 3; 24.2%), lanceolate (score 5; 6.1%), lobulated (score 6; 57.6%) and almost divided (score 7; 12.1%). Leaf length ranged from 7.4 to 29.4 cm for clone CL 18 and Rainha da Praia, respectively, in which 69.7% of the genotypes had leaves classified as medium (8 to 15 cm; Huamán, 1991). In addition to being an important characteristic, which is linked to leaf area, photosynthetic capacity and yield, when used in human food it can contribute to health, based on its nutritional composition and the presence of bioactive compounds, which act as anti-inflammatory agents, which promote resistance to cancer, prevent vascular and neurodegenerative diseases, such as Alzheimer's and Parkinson's (Silva-Correa et al., 2022). In ruminant feed, it contributes quality roughage, and can be included in the diet, without reducing animal productivity rates (Gupta et al., 2018).

There were five types of vein pigmentation, with a predominance of green (score 2; 51.5%), but also purple color patterns (Table 1), such as rock spots on several veins (score 3; 3.1%), purple main vein (score 5; 9.1%), all veins partially purple (score 7; 12.1%) and all veins totally purple (score 8; 24.2%). The color pattern of the mature leaf followed the color of the main branch, ranging from green (32 genotypes) to purple (Pão variety). For immature leaf color, in addition to the characteristic green in 54.5% of the genotypes (score 2), there were green leaves with purple tips (score 3; 39.4%) and a soft purple pattern (score 6, 6.1%).

The petiole is responsible for attaching the leaf to the branch and its length can help in the greater or lesser permeability of light at the base of the plant. For this characteristic, five classes were observed (Table 1), with the short type standing out in 75.8% of the genotypes (score 3, between 10 – 20 cm), in addition to the very short (score 1, < 10 cm; 3.0%), intermediate (score 5, between 21 and 30 cm; 15.2%), long (score 7, between 31 and 40 cm; 3.0%) and very long (score 9, > 40 cm; 3.0%), according to Huamán (1991).

Variation was observed in the type, number and shape of the leaf lobes, which, because it is an easily identifiable characteristic, can be used to differentiate hybrids from parents. Also, in high-density plantations, combined with the length of the petiole and leaf shape, the higher number of lobules can improve ventilation and allow more light to reach the base of the plant, increasing light absorption (Ni et al., 2014). The types of lobes observed were very soft (score 1; 24.2%), moderate (score 5; 60.6%) and deep (score 7; 15.2%). Regarding the number, leaves without lobes (24.2%), with three (54.5%) and five lobes (21.2%), with a shape classified as toothed (score 1; 21.2%), triangular (score 2, 6.1%), semi-elliptical (score 4; 60.6%) and elliptical (score 5; 12.1%).

For the quantitative root traits, the coefficient of variation ranged from 22.6% for root length to 69.1% for weight (Table 2), indicating wide variation in the dataset that may be related to the genetic variability of the collection (Cavalcante & Costa, 2021). Root weight ranged from 42 g (family F-05) to 2,082 g (clone CL 28), in which 18 genotypes weighed more than 500 g/plant. On the other hand, the number of roots reached up to 14 units (Bem Cuia variety). The root diameter ranged from 17.2 to 103.3 mm, for the varieties Copinha Rosa and clone CL 28, respectively. The Copinha Rosa variety had the longest root length. These variables are important tools when analyzing the commercial interest of producers and consumers.

Table 2.

Root morphological characteristics of sweet potato genotypes

Genotypes	RW (g)	RN	RD (mm)	RL (cm)	CT (mm)	RS	SD	EC	PC	PL	ID
Amendoim	668	10	32.2	15.0	2.2	8	3	5Y-6/2	5Y-7/2	5	1
Bem Cuia	760	14	40.5	13.4	4.8	3	5	5R-3/6	7.5Y–8/4	5	1
Beterraba 1	318	5	44.8	10.9	1.8	3	3	5R-1/6	7.5RP-4/4	3	0
Campinas 1	454	6	38.7	14.3	3.6	8	3	2.5R-2/6	10Y-8/2	5	0
Campinas 2	882	4	52.7	15.3	3.4	4	3	10RP-4/6	7.5Y-9/4	5	1
Canela	604	3	39.4	9.9	1.9	3	3	7.5R-5/4	5Y-8/4	3	0
CL 10	74	3	20.4	8.9	1.3	9	3	10R-4/8	10Y-8/4	5	1
CL 15	1,420	4	64.4	13.8	3.0	4	3	5R-4/8	10Y 8/4	5	1
CL 17	484	5	43.1	14.3	3.2	8	3	10R 3/4	10Y-8/2	5	1
CL 18	722	3	76.6	10.8	2.4	2	5	2.5YR-5/6	10Y-8/4	3	3
CL 22	382	4	57.3	15.2	2.8	7	3	10R-5/4	7.5Y-7/4	5	1
CL 26	1,138	8	48.4	11.9	4.0	4	3	7.5R-2/4	7.5Y-9/4	5	0
CL 28	2,082	4	103.3	8.5	2.0	1	5	5Y-5/2	5Y-8/2	5	1
CL 31	100	1	40.0	9.9	2.2	7	3	2.R-4/8	10Y-8/2	5	0
CL 39	1,182	3	76.0	13.6	2.4	2	5	7.5R-8/4	7.5Y-8/2	5	1
CL 40	402	2	53.8	9.8	3.9	3	3	2.5YR-2/6	5Y-7/6	5	0
Cop. Rosa	59	1	17.2	23.4	1.4	9	3	7.5R-5/4	7.5Y-7/4	5	0
F-01	796	3	37.1	14.8	1.5	8	3	5Y-8/4	2.5G-8/2	3	5
F-04	398	3	64.0	15.3	3.5	3	3	10YR-4/4	5Y-8/4	5	1

F-05	42	2	17.5	8.9	2.8	9	3	2.5YR 4/6	10Y 8/4	5	1
F-09	812	3	48.2	12.7	2.8	4	3	2.5Y-6/4	7.5Y-6/4	5	1
F-10	420	5	44.3	13.4	2.7	9	3	5YR-5/2	7.5Y-9/2	5	1
F-11	562	4	49.5	11.4	1.7	4	3	2.5YR-3/6	7.5Y-8/4	5	1
F-14	500	2	87.0	11.9	4.1	6	5	2.5Y-8/4	7.5Y-8/4	5	0
F-15	1,250	4	80.0	9.9	1.8	1	5	7.5Y-8/2	7.5Y-7/2	5	1
F-16	1,668	6	64.3	13.4	2.6	4	3	2.5R-4/8	10Y-9/2	5	0
Gaia	232	2	36.4	8.9	3.0	5	3	2.5Y-6/4	5Y-7/4	5	1
M. Família	240	2	50.0	15.0	4.0	3	3	10YR-4/4	10Y-7/2	1	1
Pão	510	5	30.7	12.2	2.8	9	3	10YR-6/6	2.5GY-8/2	5	1
R. Praia	330	2	60.1	12.0	3.8	9	3	10YR-6/4	7.5Y-7/2	5	1
R. Penedo	716	5	37.2	12.5	5.2	9	3	5Y-7/4	10Y-7/2	3	1
Roxinha	496	6	41.3	13.6	2.9	3	3	5R-4/4	2.5GY-9/2	5	1
Tinguá	862	4	28.0	15.3	2.6	9	3	5R-6/8	10Y-8/4	5	1
CV (%)	69.1	62.3	40.3	22.6	33.9	51.3	23.3	--	--	--	--

Note: RW: root weight; NR: root number; RD and RL: root diameter and length; CT: cortex thickness; RS: root shape; SD: surface defect; EC and PC: epidermis and pulp color; PL: presence of latex; ID: incidence of pest damage. CV (%): coefficient of variation.

There was variation in the thickness of the root cortex, classified as thin (between 1 - 2 mm; 21.2%), intermediate (between 2 - 3 mm; 39.4%), thick (between 3 - 4) and very thick (> 4 mm) for 21.2 and 15.2% of the genotypes, respectively (Table 2). There was wide phenotypic variability for the root shape variable, identifying all nine types of classification present in the species (Huamán, 1991), with a predominance of curved (score 9; 24.2%), elliptical (score 3; 21.2%) and oval (score 4; 18.2%) shapes, with the presence of shallow horizontal constrictions (score 3; 81.8%) and shallow longitudinal folds (score 5; 18.2%).

The colorations of the epidermis and the pulp of the roots presented five types of classes each, considering the color classification established by Munsell (1975), with a predominance of pinkish (48.5%), cream (24.2%) and red (15.2%). The cream (45.5%) and white (36.4%) colors of the fresh pulp predominated, with the purple color standing out in the Beetroot 1 variety, indicating a strong concentration of anthocyanins, with their antioxidant properties (Silva-Correa et al., 2022). Root color, in general, is an important characteristic linked to consumer preference (Evangelista et al., 2022), being associated with polyphenol contents, i.e., roots with lighter colors have low levels (Wen-Ging et al., 2023). The genotypes were classified as low latex (score 3; 3.0%), some (score 5; 15.2%) and abundant (score 7; 81.8%). Regarding the variable incidence of pest damage, 93.0% of the genotypes showed mild damage, not causing interference in commercialization.

Morphological descriptors provide the phenotypic pattern of the genotypes of a collection and are used as a tool to estimate genetic variability. In this sense, from the 25 descriptors evaluated, using the Tocher clustering method, it was possible to observe the formation of six groups of similarity (Table 3), evidencing the existence of genetic divergence among the 33 sweet potato genotypes. The cophenetic correlation coefficient was 0.70**, indicating that the test was robust in summarizing the information in the dissimilarity matrix, i.e., less information loss.

Table 3.

Grouping established by the multivariate Tocher method among 33 sweet potato genotypes evaluated by 25 morphological characteristics of the shoot and roots

Groups	Genotypes
I	Amendoim, Bem Cuia, Campina 1, Campina 2, Canela, CL 10, CL 15, CL 22, CL 26, CL 39, F-01, F-04, F-05, F-09, F-10, F-14, F-16, Gaita, Rainha de Penedo
II	Beterraba 1, CL 17, CL 31, CL 40, F-11, Mãe de Família, Tinguá, Copinha Rosa
III	CL 18, F-15
IV	Pão, Roxinha
V	CL 28
VI	Rainha da Praia

Group I consisted of nine genotypes (Table 3). The highest Gower distance (0.48) was observed between the Beterraba 1 and Rainha da Praia landraces, being the most heterogeneous among the genotypes studied. On the other hand, the shortest distance (0.041) was observed between the F-11 and Tinguá genotypes, with high similarity, which may indicate the existence of duplicates or genotypes with a high degree of kinship. The greater the distance of the genotypes, the greater the hybrid vigor (Bali et al., 2022).

Considering not only the Gower distances, but also the phenotypic characteristics of the genotypes, aiming gains with greater heterosis and superior progenies, we propose biparental crosses between ‘CL 28 x Beterraba 1’ (hybrid: short internode; number and weight of the root; purple coloration for epidermis and pulp), ‘CL 28 x Pão’ (hybrid: purple leaf; number and weight of the root; light coloration for epidermis and pulp), ‘CL 15 x Beterraba 1’ (hybrid: short internodes; root weight; light epidermis and purple pulp), ‘CL 15 x Pão’ (hybrid: purple leaf; root weight; light colouring for epidermis and pulp), ‘CL 28 x F-16’ (hybrid: root weight; light-coloured epidermis and pulp), ‘CL 15 x F-16’ (hybrid: root weight; dark coloured and light cream epidermis and pulp, respectively), ‘CL 28 x F-15’ (hybrid: short internode; root weight; light-coloured epidermis and pulp), ‘CL 15 x F-15’ (hybrid: short internode; root weight; epidermis and purple and cream pulp, respectively), ‘F-15 x Beterraba 1’ (hybrid: root weight; light epidermis and purple pulp), ‘F-16 x Beterraba 1’ (hybrid: number of roots; epidermis and purple pulp), ‘F-15 x Pão’ (hybrid: purple leaf; root weight; epidermis and light pulp), ‘F-16 x Pão’ (hybrid: purple leaf; number and weight of roots; epidermis and pulp with purple and light hue, respectively).

Conclusion

The morphological descriptors of the shoot and roots showed the existence of genetic divergence between the genotypes evaluated, allowing the indication of the biparental crosses ‘CL 28 x Beterraba 1’, ‘CL 28 x Pão’, ‘CL 15 x Beterraba 1’, ‘CL 15 x Pão’, ‘CL 28 x F-16’, ‘CL 15 x F-16’, ‘CL 28 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x F-15’, ‘CL 15 x

F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 15 x F-15', 'CL 'F-15 x Beterraba 1', 'F-16 x Beterraba 1', 'F-15 x Pão', 'F-16 x Pão'. As a result, they enable gains with greater heterosis and superior progenies.

REFERENCES

Austin, D. F. (1987). The taxonomy, evolution and genetic diversity of sweet potatoes and related wild species. In: International Potato Center (Org.). *Exploration, maintenance and utilization of sweet potato genetic resources*. (pp.27-59). International Potato Center.

Azevedo, A. M., Andrade Júnior, V. C., Figueiredo, J. A., Pedrosa, C. E., Viana, D. J. S., Lemos, V. T., Neiva, I. P. (2019). Genetic divergence and importance of traits in sweet potato genotypes for silage production. *Brazilian Journal of Agrarian Sciences,* 10(3), 479-484. DOI: https://doi.org/10.5039/agraria.v10i3a5165.

Bali, B., Thakur, P., Kar, S., Kumar, Y. (2022). Estimation of genetic divergence in Sweet Potato [*Ipomea batatas* (L.)] for tuber yield and it's attributing traits. *The Pharma Innovation Journal*, 11(2), 2530-2533.

Bovell-Benjamin, A. C. (2007). Sweet potato: a review of its past, present, and future role in human nutrition. *Advances in Food and Nutrition Research,* 52(1), 1-59. DOI: https://doi.org/10.1016/S1043-4526(06)52001-7.

Cavalcante, M., Ferreira, P. V., Paixão, S. L., Madalena, J. A da S., Pereira, R. G. (2008). Characterization and genetic divergence of sweet potato by means of morphological markers. *Caatinga Magazine*, 21(4), 89-85.

Cavalcante, M., Ferreira, P. V., Paixão, S. L., Costa, J. G. da, Pereira, R. G., Madalena, J. A. da S. (2009). Productive and genetic potential of sweet potato clones. *Acta Scientiarum.Agronomy*, 31(3), 421-426. DOI: https://doi.org/10.4025/actasciagron.v31i3.835.

Cavalcante, M., Costa, J. G. (2021). Considerations on experimental design and statistical methods in Agricultural Sciences. *Diversitas Journal,* 6(4), 3706-3723. DOI: https://doi.org/10.48017/dj.v6i4.1931.

Climate-Date. (2023). *Maragogi/AL - Brazil.* Available at: <https://pt.clima-date.org/america-do-sul/brasil/alagoas/maragogi-43113/>. Accessed on: June 12, 2023.

Cruz, C. D. (2013). GENES - Software for data analysis in experimental statistics and quantitative genetics. *Acta Scientiarum.Agronomy*, 35(3), 271–276. DOI: https://doi.org/10.4025/actasciagron.v35i3.21251.

Cruz, C. D., Ferreira, F. M., Pessoni, L. A. (2020). *Biometrics applied to the study of genetic diversity*. Viçosa: UFV. 626p.

Evangelista, R. L. C. A., Silva, J. da, Gomes, J. A., Weirich Neto, P. H., Souza, N. M. (2022). Morphological characterization of 21 sweet potato genotypes. *AgroFIB Journal*, 2(1), 55-66. DOI: https://doi.org/10.59237/agrofib.v2i.499.

FAO: Food and Agriculture Organization of the United Nations. (2020). *FAOSTAT: Sweet potato*. Available at: <https://www.fao.org/faostat/en/#data/QI>. Accessed on: 01 May. 2023.

Fernandes, A. M., Melo, A. F. S., Moura, A. P. de, Lopes, C. A., Echer, F R. (2021). *Sweet Potato Production System*. Brasilia: Embrapa Vegetables. 66p.

Ferreira, P. V. (2018). Estatística Experimental Aplicada às Ciências Agrárias. Viçosa: Editora UFV. 588p.

Gupta, S., Pareek, S., Ameta, K. D., Sarolia, D. K., Pilania, S., Kaushik, R. A.Kumari, P. (2018). Analysis of nutritional composition of sweet potato vines. *Journal of Pharmacognosy and Phytochemistry*, 7(2), 104-106.

Huamán, Z. (1991). *Descriptors for sweet potato*. Rome: International Board for Plant Genetic Resources. 52p.

IBGE: Brazilian Institute of Geography and Statistics. (2020a). *Census of Agriculture: Table 6953 – updated on 08/06/2020*. Available at: <https://sidra.ibge.gov.br/tabela/6953>. Accessed on: 01 May. 2023.

IBGE: Brazilian Institute of Geography and Statistics. (2020b). *Census of Agriculture: Table 6852 – updated on 08/06/2020*. Available at: <https://sidra.ibge.gov.br/tabela/6852>. Accessed on: June 17, 2023.

Indriani, F. C., Restuono, J., Rahajeng, W., Iswanto, R., Sundari, T., Soehendi, R., Harnowo, D., Baliadi, Y., Mejaya, M. J. (2021). Clone x Tester Crosses on compatibility level of sweetpotato (*Ipomoea batatas* L.). *Annual Research & Review in Biology*, 36(5), 23-37. DOI: https://doi.org/10.9734/arrb/2021/v36i530372

Melo, R. A. de C., Amaro, G. B., Vendrame, L. P. de C., Pilon, L. (2019). *Yield of sweet potato in beds using different spacing and branch segments*. Brasilia: Embrapa Vegetables. 20p.

Munsell Soil Color Company. (1975). *Munsell soil color charts*. Baltimore: Munsell Color. 117p.

Nguyen, H. C., Chen, C., Lin, K., Chao, P., Lin, H., Huang, M. (2021). Bioactive compounds, antioxidants, and health benefits of sweet potato leaves. *Molecules*, 26(7), 1-13. DOI: https://doi.org/10.3390/molecules26071820

Ni, X., Huang, J., Ali, B., Zhou, W., Zhao, J. (2015). Genetic analysis and fine mapping of the LOBED-LEAF 1 (BnLL1) gene in rapeseed (*Brassica napus* L.). *Euphytica*, 204(1), 29-38. DOI: https://doi.org/10.1007/s10681-014-1319-6.

Ritschel, O. S., Thomazelli, L. F., Huáman, Z. (1998). *Morphological characterization of sweet potato germplasm maintained by EPAGRI*. Brasilia: Embrapa Vegetables. 7p.

Perrud, A. C., Bavaresco, L. G., Zeist, A. R., Leal, M. H. S., Silva Júnior, A. D. S., Resende, J. T. V. de, Silva, M. L. da, Toroco, B. R. (2021). Relationship between bud number in seed branches and yield aspects of sweet potato. *Horticultura Brasileira,* 39(4), 451-457. DOI: https://doi.org/10.1590/s0102-0536-20210415.

Silva-Correa, C. R., Hilario-Vargas, J., Torre, V. E. V., Calderón-Peña, A. A., González-Siccha, A. D., Aspajo-Villalaz, C. L., Cruzado-Razco, J. L. (2022). Potential Anticancer Activity of Bioactive Compounds from *Ipomoea batatas*. *Pharmacognosy Journal*, 14(3), 650-659. DOI: https://doi.org/10.5530/pj.2022.14.84.

Silva, G. O., Ponijaleki, R., Suinaga, F. A. (2012). Genetic divergence between sweet potato accessions using root phenotypic traits. *Horticultura Brasileira*, 30(4), 595-599. DOI: https://doi.org/10.1590/S0102-05362012000400006.

Silva, G. O., Suinaga, F. A., Ponijaleki, R., Amaro, G. B. (2015). Performance of sweet potato cultivars for traits related to root yield. *Ceres Journal,* 62(4), 379-383. DOI: https://doi.org/10.1590/0034-737X201562040007.

Srisuwan, S., Sihachakr, D., Siljak-Yakovlev, S. (2006). The origin and evolution of sweet potato (*Ipomoea batatas* Lam.) and its wild relatives through the cytogenetic approaches. *Plant Science*, 171(3), 424-433. DOI: https://doi.org/10.1016/j.plantsci.2006.05.007.

Wen-Ging, T., Xin-Bo, G., Zhang-Ying, W., Rong, Z., Chao-Chen, T., Bing-Zhi, J., Rui-Xue, J., Yuan-Yuan, D., Shao-Hai, Y., Jing-Yi, C. (2023). Metabolic profile and morphological characteristics of leaf tips among different sweet potato (*Ipomoea batatas* Lam.) varieties. *Journal of Integrative Agriculture*, 25(1), 1-20. DOI: https://doi.org/10.1016/j.jia.2023.04.029.